



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: de la Monte, Suzanne
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 - (B) STREET: 1100 New York Ave., Suite 600
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Esmond, Robert W.
 - (B) REGISTRATION NUMBER: 32,893
 - (C) REFERENCE/DOCKET NUMBER: 0609.4370000
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 15..1139
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC
Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys

1

5

10

AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser	98
15 20 25	
GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys	146
30 35 40	
ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe	194
45 50 55 60	
CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro	242
65 70 75	
TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala	290
80 85 90	
CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met	338
95 100 105	
TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu	386
110 115 120	
CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile	434
125 130 135 140	
TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val	482
145 150 155	
CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys	530
160 165 170	
CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His	578
175 180 185	
CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln	626
190 195 200	
AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly	674
205 210 215 220	
TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser	722
225 230 235	
CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe	770
240 245 250	
TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile	818
255 260 265	
TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT	866

Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala			
270	275	280	
Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys			914
285	290	295	300
TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG			962
Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp			
305	310	315	
CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC			1010
Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe			
320	325	330	
TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA			1058
Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro			
335	340	345	
CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT			1106
His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr			
350	355	360	
TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT			1159
Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg			
365	370	375	
TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA			1219
AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCAGGC TGGTCTCAA CTTCTGGCTT			1279
CATGCAATCC TTCCAAATGA GCCACAAACAC CCAGCCAGTC ACATTTTTAACAGTTACA			1339
TCTTTATTTT AGTACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA			1399
GTAACAGAGT TCTTTATAA CTTTAAACA AAGCTTTAGA GCA			1442

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile			
1	5	10	15

Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala			
20	25	30	

Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg			
35	40	45	

Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly			
50	55	60	

Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala			
65	70	75	80

Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu

85

90

95

Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	Cys	Pro	Ser	Trp
100								105					110		
Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu	Pro	Lys	Cys	Trp
115							120					125			
Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile	Leu	Phe	Phe	Leu
130						135					140				
Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val	Gln	Trp	Cys	Asp
145					150					155			160		
His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	His	Pro	Pro	Ala
165						170					175				
Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His	His	Tyr	Thr	Trp
180							185					190			
Leu	Ile	Phe	Ile	Phe	Ile	Phe	Asn	Phe	Leu	Arg	Gln	Ser	Leu	Asn	Ser
195							200					205			
Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Arg	Asn	Leu	Gly	Ser	Leu	Gln	Pro
210						215					220				
Leu	Pro	Pro	Gly	Phe	Lys	Leu	Phe	Ser	Cys	Pro	Ser	Leu	Leu	Ser	Ser
225					230					235			240		
Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe	Phe	Val	Phe	Leu
245							250					255			
Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile	Leu	Ile	Ser	Gly
260						265					270				
Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Gly	Ile	Thr	Gly
275							280					285			
Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe	Asn	Phe	Cys	Leu	Phe	Glu	Met
290						295					300				
Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Pro	Asn	Leu	Gly
305						310				315			320		
Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe	Ser	Cys	Leu	Ser
325							330					335			
Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Gly	His	Leu	Pro	Pro	His	Pro	Ala	Asn
340							345					350			
Phe	Cys	Ile	Phe	Ile	Arg	Gly	Gly	Val	Ser	Pro	Tyr	Leu	Ser	Gly	Trp
355							360					365			
Ser	Gln	Thr	Pro	Asp	Leu	Arg									
370						375									

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT 60
CTCAGCTCAC CGCAACCTCC GCCTCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTTTAGTA 180
GAGATGGAGT TTAACTCCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC 240
TCCCGTCTCG GCCTGCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC 300
TGCCTGGCTA ATTTTTGTGG TAGAACACAGG GTTTCACTGA TGTTGCCAA GCTGGTCTCC 360
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCGTCAGCC 420
GTGCCTGGCC TTTTTTATTAA ATTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT 480
GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTCAA CTCCTGAGAT CAAGCAATCC 540
TCCTGCCTCA GCCTCCCAAG TAGCTGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600
TTTATTTAA TTTTTAATTAA TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC 660
AGTGGCGCAA TCTGGCTCA CTGCAACCTC TGCTCCGG GTTCAAGTTA TTCTCCTGCC 720
CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTGTAT 780
TTTTAGTAGA GATGGGGTTT CACCATGTTG GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840
GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC 900
CTATTTTAA TTTTGTTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960
AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCGGG TCAAGCGATT CTCCTGTCTC 1020
AGCCTCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTT 1080
CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACTCCTGA CCTCAGGTGA 1140
CCCACCTGCC TCAGCCTTCC AAAGTGTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200
GGCTAATTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
TCAAACCTCT GGCTTCAGTC AATCCTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320
TTTTAACACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380
C 1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT 60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTAGT 180
AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT 240
CCCGTCTCGG CCTCCCAAAG TGCTAGATAAC AGGACTGAGC ACCATGCCCG GCCTCTGCCT 300
GGCTAATTTC TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT 360
CAAGCAGTCC ACCTGCCTCA GCCTCCAAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC 420
TGGCCTTTT ATTATTTTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT 480
GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC 540
TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTAT 600
TTTTATTTT AATTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG 660
GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTTC AAGTTATTCT CCTGCCCGAG 720
CCTCCTGAGT AGCTGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTT TTGTATTTTT 780
AGTAGAGATG GGGTTTCACC ATGTTCGCCA GGTTGATGCT AGATCTCTTG ACCTTGTGAT 840
CTGCCTGCCT CGGCCTCCC AAGTGCTGGG ATTACAGGAC GTGACGCCA CCGCCCGGCC 900
TATTTTAAT TTTTGTGTGTT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA 960
ATGGCCAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT 1020
CAGCCTCCC AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCCGCTAA TTTTTGTATT 1080
TTCATTAGAG GCGGGGTTTC ACCATATTG TCAGGCTGGT CTCAAACCTCC TGACCTCAGG 1140
TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GGCGTGACGC CTCACCCAGC 1200
CGGCTAATT AGATAAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG 1260
GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACCC AGCCAGTCAC 1320
ATTTTTAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG 1380
AACCTGCAAAT TTCGAGTAGT ACAGAGTCTT TTATAACT 1418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGGCAG ATCACAAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14